

The following Listing of the Claims will replace all prior versions and all prior listings of the claims in the present application:

Listing of The Claims:

- 1-42. (Cancelled)
43. (Currently Amended) A chimeric expression promoter comprising at least one nucleic acid sequence ~~derived from~~ comprising a Commelina Yellow Mottle Virus first plant promoter originating from a Commelina Yellow Mottle Virus comprising wherein a plant vascular expression promoter region of said Commelina Yellow Mottle Virus plant promoter, said plant vascular expression promoter region being is replaced with a nucleic acid sequence ~~derived from a second~~ comprising a Cassava Vein Mosaic Virus plant promoter originating from a Cassava Vein Mosaic Virus comprising a plant green tissue expression promoter region.
44. (Currently Amended) The chimeric expression promoter of claim 43, wherein said nucleic acid sequences originate from the intergenic regions of said ~~first and second~~ Commelina Yellow Mottle Virus and Cassava Vein Mosaic Virus plant promoter.
45. (Currently Amended) The chimeric expression promoter of claim 43, comprising ~~at least a part of~~ the nucleic acid sequence of SEQ ID NO: 1, but not including a plant vascular expression promoter region of said SEQ ID NO: 1 fused to at least a part of the a nucleic acid sequence comprising a plant green tissue expression promoter region of SEQ ID NO: 2.
46. (Previously presented) The chimeric expression promoter of claim 43, wherein the nucleic acid sequence of said chimeric expression promoter consists of a sequence selected from the group consisting of the sequences with SEQ ID NOS: 3-7 and 19-25.
47. (Previously presented) The chimeric expression promoter of claim 43, further comprising at least one endosperm like box.

48. (Previously presented) The chimeric expression promoter of claim 43, further comprising at least one as1 like box operably linked to a plant green tissue expression GT promoter element.
49. (Previously presented) The chimeric expression promoter of claim 43, further comprising at least one as1 box operably linked to a green tissue expression GT promoter element.
50. (Currently Amended) The chimeric expression promoter of claim 43, further comprising at least one as2 box operably linked to a plant green tissue expression ϵ GT promoter element.
51. (Currently Amended) The chimeric expression promoter of claim 43, comprising at least one as1 like, as1, and as2 box operably linked upstream or downstream to the plant green tissue expression ϵ GT promoter element.
52. (Previously presented) The chimeric expression promoter of claim 43, comprising at least one as1 like, as1, and as2 box operably linked in 5' to 3' or 3' to 5' orientation.
53. (Previously presented) The chimeric expression promoter of claim 43, comprising at least one as2/as2/as2 box in 5' to 3' or 3' to 5' orientation.
54. (Currently Amended) A chimeric expression promoter comprising a ~~first Commelina Yellow Mottle Virus promoter of viral origin, originating from a Commelina Yellow Mottle Virus~~, of which ~~a part consists of an~~ a plant vascular expression promoter region is replaced with an exogenous Cassava Vein Mosaic Virus element ~~of viral origin which promotes expression in plant green tissues and originates from a Cassava Vein Mosaic Virus~~.
55. (Previously presented) The chimeric expression promoter of claim 54, further comprising at least one endosperm like box.
56. (Previously presented) The chimeric expression promoter of claim 54, further comprising at least one as1 like box operably linked to a plant green tissue expression GT promoter element.

57. (Previously presented) The chimeric expression promoter of claim 54, further comprising at least one as1 box operably linked to a green tissue expression GT promoter element.
58. (Previously presented) The chimeric expression promoter of claim 54, further comprising at least one as2 box operably linked to a plant green tissue expression GT promoter element.
59. (Previously presented) The chimeric expression promoter of claim 54, comprising at least one as1 like, as1, and as2 box operably linked upstream or downstream to the plant green tissue expression GT promoter element.
60. (Previously presented) The chimeric expression promoter of claim 54, comprising at least one as1 like, as1, and as2 box operably linked in 5' to 3' or 3' to 5' orientation.
61. (Previously presented) The chimeric expression promoter of claim 54, comprising at least one as2/as2/as2 box in 5' to 3' or 3' to 5' orientation.
62. (Previously presented) The chimeric expression promoter of claim 54, comprising at least one sequence selected from the group consisting of the sequences of SEQ ID NOS: 3-7 and 19-25.
63. (Currently amended) An expression cassette comprising at least one first nucleic acid sequence ~~derived from comprising a Commelina Yellow Mottle Virus~~ first plant promoter originating from a Commelina Yellow Mottle Virus comprising wherein a plant vascular expression promoter region of said Commelina Yellow Mottle Virus plant promoter, said plant vascular expression promoter region being is replaced with a second nucleic acid sequence ~~derived from a second comprising a Cassava Vein Mosaic Virus~~ plant promoter originating from a Cassava Vein Mosaic Virus and comprising a plant green tissue expression promoter region, said at least one nucleic acid sequence being operably linked to a third nucleic acid sequence or gene coding for a polypeptide to be produced, said third nucleic acid sequence or gene itself operably linked to a transcription termination nucleic acid sequence.

64. (Currently Amended) The expression cassette of claim 63, wherein the at least one nucleic acid sequence comprises ~~at least a part of~~ the nucleic acid sequence of SEQ ID NO: 1, but not including a plant vascular expression promoter region of said SEQ ID NO: 1 fused to at least a part of the a nucleic acid sequence comprising a plant green tissue expression promoter region of SEQ ID NO: 2.
65. (Previously presented) The expression cassette of claim 63, comprising a nucleic acid sequence selected from the group consisting of the sequences of SEQ ID NOS: 3-7 and 19-25, said nucleic acid sequence being operably linked to a nucleic acid sequence or a gene encoding for a polypeptide to be produced, said nucleic acid sequence or gene operably linked to a transcription termination nucleic acid sequence.
66. (Currently amended) An isolated promoter nucleic acid sequence comprising a fusion of ~~at least a part of each of~~ the sequences of SEQ ID NO: 01, but not including a plant vascular expression promoter region of said SEQ ID NO: 01, and a nucleic acid sequence comprising a plant green tissue expression promoter region of SEQ ID NO: 02.
67. (Previously presented) The isolated promoter nucleic acid sequencer of claim 66, corresponding to any one of the sequences set forth in SEQ ID NO: 03, SEQ ID NO: 04, SEQ ID NO: 05, SEQ ID NO: 06, SEQ ID NO: 07, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, and SEQ ID NO: 25.
68. (Previously presented) A vector comprising an isolated promoter nucleic acid sequence which initiates transcription of a nucleic acid sequence coding for a polypeptide, wherein said isolated promoter nucleic acid sequence comprises a chimeric expression promoter nucleic acid sequence according to claim 43, 54, or 67.
69. (Previously presented) The vector of claim 68, wherein said vector is selected from the group consisting of the binary vectors pMRT1152, pMRT1171, pMRT1172, pMRT1185, pMRT1186, pMRT1187, pMRT1188, pMRT1182, pMRT1245, pMRT1246, pMRT1247,

pMRT1248, pMRT1249, pMRT1250, pMRT1251, pMRT1252, pMRT1253 and pMRT1254.

70. (Previously presented) A transgenic plant comprising at least one stably integrated promoter nucleic acid sequence according to claim 43, 54, or 67.
71. (Previously presented) The transgenic plant of claim 70, wherein said plant is a dicotyledonous species selected from the group consisting of potato, tobacco, cotton, lettuce, tomato, melon, cucumber, pea, rape, beetroot, and sunflower, or from a monocotyledonous species selected from the group consisting of wheat, barley, oat, rice, and corn.
72. (Previously presented) A propagule of the transgenic plant according to claim 71.
73. (Previously presented) The propagule of claim 72, wherein the propagule is a seed.
74. (Previously presented) A cell containing a promoter nucleic acid sequence according to claim 43, 54, or 67, wherein said cell is selected from the group consisting of a plant cell, human cell, animal cell, insect cell, bacterial cell, yeast cell, fungal cell, algal cell, and microalgal cell.
75. (Previously presented) The cell of claim 74, wherein the cell is a plant cell.
76. (Previously presented) A method for expressing a nucleic acid sequence coding for a polypeptide by a cell, wherein said method comprises:
 - (a) transforming said cell with a vector comprising at least one promoter nucleic acid sequence according to claim 43, 54, or 67; and
 - (b) culturing said cell and expressing said polypeptide encoded by said sequence in said cell.
77. (Previously presented) The method of claim 76, wherein said cell is a prokaryotic or an eukaryotic cell.

78. (Previously presented) The method of claim 77, wherein said cell is a cell selected from the group consisting of bacterial cells, fungal cells, yeast cells, insect cells, human cells, animal cells, algal cells, microalgal cells and plant cells.

79. (Previously presented) The method of claim 76, wherein said cell is a plant cell.

80. (Previously presented) A method for manufacturing a transgenic plant or a propagule of said transgenic plant, wherein said method comprises:

(a) transforming a plant cell with a vector comprising at least one promoter nucleic acid sequence according to claim 43, 54, or 67;

(b) selecting said plant cell comprising said promoter nucleic acid sequence; and

(c) propagating said selected plant cell by culture or by regeneration of whole chimeric or transgenic plants.

Respectfully submitted,

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